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IN THE SPECIFICATION:

At page 18, lines 7-9, please amend as follows:

A1 Software for performing BLAST analyses is publicly available, e.g., through the National Center for Biotechnology Information ~~(http://www.ncbi.nlm.nih.gov/)~~ , U.S. National Library of Medicine, 8600 Rockville Pike, Bethesda, MD 20894.

At page 52, lines 21-27, please amend as follows:

A2 Gene identities can be determined by conducting BLAST (Basic Local Alignment Search Tool; Altschul, S. F., et al., (1993) J. Mol. Biol. 215:403-410; ~~see also www.ncbi.nlm.nih.gov/BLAST/~~) searches under default parameters for similarity to sequences contained in the BLAST "nr" database (comprising all non-redundant GenBank CDS translations, sequences derived from the 3-dimensional structure Brookhaven Protein Data Bank, the last major release of the SWISS-PROT protein sequence database, EMBL, and DDBJ databases).

At page 40, lines 17-24, please amend as follows:

A3 A first DNA plasmid was constructed by combining the *ZmAxig1* promoter (661 bases 5' of the start codon; see SEQ ID NO: 3) with the Ms45 coding sequence and 35S:PAT in a T-DNA vector. This plasmid was cointegrated with Japan Tobacco plasmid pSB1 (Japan Tobacco, Inc; see U.S. Patent No. 5,981,840) to create a first suitable vector, V1.

A second DNA plasmid was constructed by combining the *ZmAxig1* promoter ~~(1307 bases 5' of the start codon)~~ (1306 bases 5' of the start codon; SEQ ID NO:16) with the Ms45 coding sequence and 35S:PAT in a T-DNA vector. This plasmid was cointegrated with Japan Tobacco plasmid pSB1 to create a second suitable vector, V2.